

SEQUENCE LISTING

<110> Wyeth
Ling, Vincent
Carreno, Beatriz M.
Collins, Mary

<120> USE OF B7-H3 TO INHIBIT LYMPHOCYTE PROLIFERATION (As Amended)

<130> 08702.6108-00000

<140> US/10/824,481

<141> 2004-04-15

<160> 35

<170> PatentIn version 3.5

<210> 1

<211> 951

<212> DNA

<213> Homo sapiens

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Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu
35 40 45

Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn
50 55 60

Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala
65 70 75 80

Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe
85 90 95

Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val
100 105 110

Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp
115 120 125

Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys
130 135 140

Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr
145 150 155 160

Val Thr Ile Thr Cys Ser Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val
165 170 175

Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr
180 185 190

Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu
195 200 205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn
 210 215 220

Pro Val Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln
 225 230 235 240

Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu Ser
 245 250 255

Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys Trp Arg
 260 265 270

Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln
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			20					25					30		

Val	Ser	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Asp	Thr	Asp	Ala	Thr	Leu
		35					40					45			

Arg	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu	Ala	Gln	Leu	Asn
	50					55					60				

Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu	Val	His	Ser	Phe	Thr
65					70					75					80

Glu	Gly	Arg	Asp	Gln	Gly	Ser	Ala	Tyr	Ser	Asn	Arg	Thr	Ala	Leu	Phe
				85						90				95	

Pro	Asp	Leu	Leu	Val	Gln	Gly	Asn	Ala	Ser	Leu	Arg	Leu	Gln	Arg	Val
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Arg	Val	Thr	Asp	Glu	Gly	Ser	Tyr	Thr	Cys	Phe	Val	Ser	Ile	Gln	Asp
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Phe	Asp	Ser	Ala	Ala	Val	Ser	Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys
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Pro	Ser	Met	Thr	Leu	Glu	Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asn	Met
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Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val
165 170 175

Phe Trp Lys Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr
180 185 190

Ser Gln Met Ala Asn Glu Arg Gly Leu Phe Asp Val His Ser Val Leu
195 200 205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn
210 215 220

Pro Val Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln
225 230 235 240

Pro Leu Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu Ser
245 250 255

Val Cys Leu Val Val Leu Leu Val Ala Leu Ala Phe Val Cys Trp Arg
260 265 270

Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln
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Asp Gly Asp Gly Glu Gly Ser Lys Thr Ala Leu Arg Pro Leu Lys Pro
290 295 300

Ser Glu Asn Lys Glu Asp Asp Gly Gln Glu Ile Ala
305 310 315

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<213> Homo sapiens

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ggcaccgatg ccacctgcg ctgctccttc tccccgagc ctggcttcag cctggcacag	840
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20 25 30

Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu
35 40 45

Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn
50 55 60

Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala
65 70 75 80

Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe
85 90 95

Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val
100 105 110

Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp
115 120 125

Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys
130 135 140

Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr
145 150 155 160

Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val
165 170 175

Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr
180 185 190

Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Ile Leu
195 200 205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn
210 215 220

Pro Val Leu Gln Gln Asp Ala His Ser Ser Val Thr Ile Thr Pro Gln
225 230 235 240

Arg Ser Pro Thr Gly Ala Val Glu Val Gln Val Pro Glu Asp Pro Val

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Glu	Pro	Gly	Phe	Ser	Leu	Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	
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Asp	Thr	Lys	Gln	Leu	Val	His	Ser	Phe	Thr	Glu	Gly	Arg	Asp	Gln	Gly	
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Ser	Ala	Tyr	Ala	Asn	Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	
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Gly	Asn	Ala	Ser	Leu	Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	
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Ser	Phe	Thr	Cys	Phe	Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	
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Ser	Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys	Pro	Ser	Met	Thr	Leu	Glu	
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Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Thr	Val	Thr	Ile	Thr	Cys	Ser	
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Ser	Tyr	Arg	Gly	Tyr	Pro	Glu	Ala	Glu	Val	Phe	Trp	Gln	Asp	Gly	Gln	
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Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met	Ala	Asn	Glu	
				405					410					415		
Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Val	Leu	Arg	Val	Val	Leu	Gly	Ala	
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Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro	Val	Leu	Gln	Gln	Asp	
		435					440					445				
Ala	His	Gly	Ser	Val	Thr	Ile	Thr	Gly	Gln	Pro	Met	Thr	Phe	Pro	Pro	
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Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu	Ser	Val	Cys	Leu	Ile	Ala	Leu	
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Leu Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys
485 490 495

Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly
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Ser Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp
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Asp Gly Gln Glu Ile Ala
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<213> Homo sapience

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Ala Leu Glu Val Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly
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Thr Asp Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser
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Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu
35 40 45

Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn
50 55 60

Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu
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Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe
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Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala
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Leu	Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu
		35					40					45			

Val	His	Ser	Phe	Xaa	Glu	Gly	Xaa	Asp	Gln	Gly	Ser	Ala	Tyr	Ala	Asn
	50					55					60				

Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala	Ser	Leu
65					70					75					80

Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe	Thr	Cys	Phe
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Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser	Leu	Gln	Val	Ala
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tggaaaagaa gaactgggtg gaaagaaata gctactctg ttcagtggtc cagaggggtc	1620
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<212> PRT
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20 25 30

Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu Cys Cys Ser
35 40 45

Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp
50 55 60

Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala Glu Gly Gln
65 70 75 80

Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu
85 90 95

Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Ala
100 105 110

Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser
115 120 125

Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met
130 135 140

Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile
145 150 155 160

Thr Cys Ser Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln
165 170 175

Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met
180 185 190

Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val Val

195																	
Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro	Val	Leu		
210						215					220						
Gln	Gln	Asp	Ala	His	Gly	Ser	Val	Thr	Ile	Thr	Gly	Gln	Pro	Met	Thr		
225					230					235					240		
Phe	Pro	Pro	Glu	Ala	Gly	Ser	Gly	Ser	Glu	Pro	Arg	Gly	Pro	Thr	Ile		
				245					250					255			
Lys	Pro	Cys	Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro	Asn	Leu	Glu	Gly	Gly		
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Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys	Asp	Val	Leu	Met	Ile		
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Ser	Leu	Ser	Pro	Ile	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Glu	Asp		
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Val	Leu	Pro	Pro	Pro	Glu	Glu	Glu	Met	Thr	Lys	Lys	Gln	Val	Thr	Leu		
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Thr	Cys	Met	Val	Thr	Asp	Phe	Met	Pro	Glu	Asp	Ile	Tyr	Val	Glu	Trp		
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Thr	Asn	Asn	Gly	Lys	Thr	Glu	Leu	Asn	Tyr	Lys	Asn	Thr	Glu	Pro	Val		
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Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu
 435 440 445

Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His
 450 455 460

Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro
 465 470 475 480

Gly Lys

<210> 11
 <211> 2324
 <212> DNA
 <213> Chimera

<400> 11
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 aacctcatct ggcagctgac agataccaaa cagctgggtgc acagctttgc tgagggccag 240
 gaccagggca gcgcctatgc caaccgcacg gccctcttcc cggacctgct ggcacagggc 300
 aacgcatecc tgaggetgca gcgcgtgcgt gtggcggaag agggcagctt cacctgcttc 360
 gtgagcatcc gggatttcgg cagcgtctgc gtcagcctgc aggtggccgc tccctactcg 420
 aagcccagca tgaccctgga gccaacaag gacctgcggc caggggacac ggtgaccatc 480
 acgtgctcca gctaccaggg ctaccctgag gctgaggtgt tctggcagga tgggcagggc 540
 gtgcccctga ctggcaacgt gaccacgtcg cagatggcca acgagcaggg cttgtttgat 600
 gtgcacagca tcctgcggtt ggtgctgggt gcaaattggc cctacagctg cctggtgcgc 660
 aaccccgctg tgcagcagga tgcgcacagc tctgtcacca tcacaccca gagaagcccc 720
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 ggcagcgctt atgccaaccg caggccctc ttcccgacc tgctggcaca aggcaatgca 960
 tccctgaggc tgcagcgcgt gcgtgtggcg gacgagggca gcttcacctg cttcgtgagc 1020

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agaagaactg ggtggaaaga aatagctact cctgttcagt ggtccacgag ggtctgcaca 2280
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<210> 12
<211> 700
<212> PRT
<213> Chimera

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<400> 12

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 20 25 30

Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu Cys Cys Ser
 35 40 45

Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp
 50 55 60

Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala Glu Gly Gln
 65 70 75 80

Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu
 85 90 95

Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Ala
 100 105 110

Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser
 115 120 125

Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met
 130 135 140

Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile
 145 150 155 160

Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln
 165 170 175

Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met
 180 185 190

Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Ile Leu Arg Val Val
 195 200 205

Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro Val Leu
 210 215 220

Gln Gln Asp Ala His Ser Ser Val Thr Ile Thr Pro Gln Arg Ser Pro
 225 230 235 240

Thr Gly Ala Val Glu Val Gln Val Pro Glu Asp Pro Val Val Ala Leu

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Phe	Ser	Leu	Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	
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	290					295					300					
Ala	Asn	Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala	
305					310					315					320	
Ser	Leu	Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe	Thr	
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Cys	Phe	Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser	Leu	Gln	
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Val	Ala	Ala	Pro	Tyr	Ser	Lys	Pro	Ser	Met	Thr	Leu	Glu	Pro	Asn	Lys	
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Gly	Tyr	Pro	Glu	Ala	Glu	Val	Phe	Trp	Gln	Asp	Gly	Gln	Gly	Val	Pro	
385					390					395					400	
Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met	Ala	Asn	Glu	Gln	Gly	Leu	
			405						410					415		
Phe	Asp	Val	His	Ser	Val	Leu	Arg	Val	Val	Leu	Gly	Ala	Asn	Gly	Thr	
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Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro	Val	Leu	Gln	Gln	Asp	Ala	His	Gly	
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Ser	Val	Thr	Ile	Thr	Gly	Gln	Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Gly	
	450					455					460					
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Lys Cys Pro Ala Pro Asn Leu Glu Gly Gly Pro Ser Val Phe Ile Phe
485 490 495

Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val
500 505 510

Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile
515 520 525

Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr
530 535 540

His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro
545 550 555 560

Ile Gln His Gln Asp Trp Met Ser Gly Lys Ala Phe Ala Cys Ala Val
565 570 575

Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro
580 585 590

Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu
595 600 605

Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp
610 615 620

Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr
625 630 635 640

Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser
645 650 655

Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu
660 665 670

Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His
675 680 685

His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
690 695 700

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<212> DNA
<213> Mouse

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acggatgcca ccctacgctg ctccctttcc ccagagcctg gcttcagtct ggcacagctc 180
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gaccaaggca gtgcctactc caaccgcaca gcgctcttcc ctgacctgtt ggtgcaaggc 300
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 tggaaaagaa gaactgggtg gaaagaaata gctactcctg ttcagtgggc cacgaggggc 1620
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<210> 14
 <211> 482
 <212> PRT
 <213> Mouse

<400> 14

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 20 25 30

Asp Pro Val Val Ala Leu Val Asp Thr Asp Ala Thr Leu Arg Cys Ser
 35 40 45

Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp
 50 55 60

Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Thr Glu Gly Arg
 65 70 75 80

Asp Gln Gly Ser Ala Tyr Ser Asn Arg Thr Ala Leu Phe Pro Asp Leu
 85 90 95

Leu Val Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Thr
 100 105 110

Asp Glu Gly Ser Tyr Thr Cys Phe Val Ser Ile Gln Asp Phe Asp Ser
 115 120 125

Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met
 130 135 140

Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asn Met Val Thr Ile
 145 150 155 160

Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val Phe Trp Lys
 165 170 175

Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met
180 185 190

Ala Asn Glu Arg Gly Leu Phe Asp Val His Ser Val Leu Arg Val Val
195 200 205

Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro Val Leu
210 215 220

Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro Leu Thr
225 230 235 240

Phe Pro Pro Glu Ala Gly Ser Gly Ser Glu Pro Arg Gly Pro Thr Ile
245 250 255

Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Glu Gly Gly
260 265 270

Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile
275 280 285

Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp
290 295 300

Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His
305 310 315 320

Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg
325 330 335

Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys
340 345 350

Ala Phe Ala Cys Ala Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu
355 360 365

Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr
370 375 380

Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu
385 390 395 400

Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp
405 410 415

Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val
420 425 430

Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu
435 440 445

Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His
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Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro
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Gly Lys

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<220>
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<222> (1)..(3)
<223> ALE, or another amino acid sequence

<220>
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<222> (7)..(17)
<223> PEDPVVALVGT, or another amino acid sequence

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<222> (26)..(27)
<223> SP, or another amino acid sequence

<220>
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<223> FAEGQDQGSAY, or another amino acid sequence

<220>
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<222> (67)..(79)
<223> ALFPDLLAQGNAS, or another amino acid sequence

<220>
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<222> (86)..(102)
<223> RVADEGSFTCFVSIRDF, or another amino acid sequence

<220>
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<222> (107)..(107)
<223> V, or another amino acid sequence

<400> 15

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Xaa Asp Ala Thr Leu Cys Cys Ser Phe Xaa Xaa Glu Pro Gly Phe Ser
20 25 30

Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu
35 40 45

Val His Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Asn
50 55 60

Arg Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu
65 70 75 80

Arg Leu Gln Arg Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Xaa Xaa Xaa Xaa Gly Ser Ala Ala Xaa Ser Leu Gln Val Ala
100 105 110

<210> 16
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<213> Artificial sequence

<220>
<223> Conserved among mammals

<400> 16

Val Gln Val
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<210> 17
<211> 8

<212> PRT
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<220>
<223> Conserved among mammals

<400> 17

Asp Ala Thr Leu Cys Cys Ser Phe
1 5

<210> 18
<211> 24
<212> PRT
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<220>
<223> Conserved among mammals

<400> 18

Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr
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Asp Thr Lys Gln Leu Val His Ser
20

<210> 19
<211> 4
<212> PRT
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<220>
<223> Conserved among mammals

<400> 19

Ala Asn Arg Thr
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<210> 20
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<212> PRT
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<220>
<223> Conserved among mammals

<400> 20

Leu Arg Leu Gln Arg Val
1 5

<210> 21
<211> 4
<212> PRT
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<220>
<223> Conserved among mammals

<400> 21

Gly Ser Ala Ala
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<210> 22
<211> 5
<212> PRT
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<220>
<223> Conserved among mammals

<400> 22

Ser Leu Gln Val Ala
1 5

<210> 23
<211> 112
<212> PRT
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<220>
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<223> L or V, or another amino acid

<220>
<221> Misc_feature
<222> (22)..(22)
<223> C or R, or another amino acid

<220>
<221> Misc_feature
<222> (53)..(53)
<223> A or T, or another amino acid

<220>
<221> Misc_feature
<222> (56)..(56)
<223> Q or R, or another amino acid

<400> 23

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Thr Asp Ala Thr Leu Xaa Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser
20 25 30

Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu
35 40 45

Val His Ser Phe Xaa Glu Gly Xaa Asp Gln Gly Ser Ala Tyr Ala Asn
50 55 60

Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu
65 70 75 80

Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe
85 90 95

Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala
100 105 110

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<211> 55

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

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<210> 25

<211> 50

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 25

ggggaccact ttgtacaaga aagctggggt caggctatatt cttgtccatc 50

<210> 26

<211> 22

<212> DNA
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 <220>
 <223> Primer

 <400> 26
 ctctggggg aatgtcatag gc 22

 <210> 27
 <211> 55
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 <220>
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 ggggacaagt ttgtacaaaa aagcaggctc caccatgctt cgaggatggg gtggc 55

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 <220>
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 <210> 30
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 <220>
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<210> 31
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ctggcacagc tcaacctcat c

21

<210> 32
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<220>
<223> Primer

<400> 32
accaggcagc tgtaggtgcc

20

<210> 33
<211> 22
<212> DNA
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<220>
<223> Primer

<400> 33
ctgtgatggt gactgagccg tg

22

<210> 34
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 34
cgcggtgcgtg tggcggatga g

21

<210> 35
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 35
tacaggaatc agcactgggt tc

22